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#2



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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/006,343

DATE: 02/01/2002
 TIME: 11:47:30

Input Set : N:\CrF3\RULE60\10006343.raw
 Output Set: N:\CRF3\02012002\J006343.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Bard, Jonathan A
 6 Borowsky, Beth
 7 Smith, Kelli E
 9 (ii) TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
 10 AND USES THEREOF
 12 (iii) NUMBER OF SEQUENCES: 65
 14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Cooper & Dunham LLP
 16 (B) STREET: 1185 Avenue of the Americas
 17 (C) CITY: New York
 18 (D) STATE: New York
 19 (E) COUNTRY: U.S.A.
 20 (F) ZIP: 10036

ENTERED

22 (v) COMPUTER READABLE FORM:
 23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:
 29 (A) APPLICATION NUMBER: US/10/006,343
 30 (B) FILING DATE: 03-Dec-2001

31 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:
 35 (A) APPLICATION NUMBER: US/09/058,333
 36 (B) FILING DATE:

40 (viii) ATTORNEY/AGENT INFORMATION:
 41 (A) NAME: White, John P
 42 (B) REGISTRATION NUMBER: 28,678
 43 (C) REFERENCE/DOCKET NUMBER: 52241-E/JPW/KDB

45 (ix) TELECOMMUNICATION INFORMATION:
 46 (A) TELEPHONE: 212 278 0400
 47 (B) TELEFAX: 212 391 0525

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:
 53 (A) LENGTH: 1280 base pairs
 54 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: single
 56 (D) TOPOLOGY: linear

58 (ii) MOLECULE TYPE: DNA

60 (ix) FEATURE:

61 (A) NAME/KEY: CDS

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62 (B) LOCATION: 63..1172
 64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 66 AGCTCCAGCC TAGGCCTTCT ACCTGGAAAGA ATGCAGGGGC CCAGTACCTA GGACTGAGGA 60
 68 AG ATG GCT GAC ATC CAG AAC ATT TCG CTG GAC AGC CCA GGG AGC GTA 107
 69 Met Ala Asp Ile Gln Asn Ile Ser Leu Asp Ser Pro Gly Ser Val
 70 1 5 10 15
 72 GGG GCT GTG GCA GTG CCT GTG ATC TTT GCC CTC ATC TTC CTG TTG GGC 155
 73 Gly Ala Val Ala Val Pro Val Ile Phe Ala Leu Ile Phe Leu Leu Gly
 74 20 25 30
 76 ATG GTG GGC AAT GGG CTG GTG TTG GCT GTG CTA CTG CAG CCT GGC CCA 203
 77 Met Val Gly Asn Gly Leu Val Leu Ala Val Leu Leu Gln Pro Gly Pro
 78 35 40 45
 80 AGT GCC TGG CAG GAG CCA AGC AGT ACC ACA GAT CTC TTC ATC CTC AAC 251
 81 Ser Ala Trp Gln Glu Pro Ser Ser Thr Thr Asp Leu Phe Ile Leu Asn
 82 50 55 60
 84 TTG GCC GTG GCC GAC CTT TGC TTC ATC CTG TGC GTG CCC TTC CAG 299
 85 Leu Ala Val Ala Asp Leu Cys Phe Ile Leu Cys Cys Val Pro Phe Gln
 86 65 70 75
 88 GCA GCC ATC TAC ACA CTG GAT GCC TGG CTC TTT GGG GCT TTC GTG TGC 347
 89 Ala Ala Ile Tyr Thr Leu Asp Ala Trp Leu Phe Gly Ala Phe Val Cys
 90 80 85 90 95
 92 AAG ACG GTA CAT CTG CTC ATC TAC CTC ACC ATG TAT GCC AGC AGC TTC 395
 93 Lys Thr Val His Leu Leu Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe
 94 100 105 110
 96 ACC CTG GCG GCC GTC TCC CTG GAC AGG TAC CTG GCT GTG CGG CAC CCA 443
 97 Thr Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala Val Arg His Pro
 98 115 120 125
 100 CTG CGC TCC AGA GCC CTG CGC ACC CCG CGC AAC GCG CGC GCC GCC GTG 491
 101 Leu Arg Ser Arg Ala Leu Arg Thr Pro Arg Asn Ala Arg Ala Ala Val
 102 130 135 140
 104 GGG CTC GTG TGG CTG CTG GCG GCT CTC TTT TCC GCG CCC TAC CTA AGC 539
 105 Gly Leu Val Trp Leu Leu Ala Ala Leu Phe Ser Ala Pro Tyr Leu Ser
 106 145 150 155
 108 TAT TAC GGC ACG GTG CGC TAC GGC GCG CTC GAG CTC TGC GTG CCC GCT 587
 109 Tyr Tyr Gly Thr Val Arg Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala
 110 160 165 170 175
 112 TGG GAG GAC GCG CGG CGG CGC GCG CTG GAC GTG GCC ACC TTC GCC GCG 635
 113 Trp Glu Asp Ala Arg Arg Ala Leu Asp Val Ala Thr Phe Ala Ala
 114 180 185 190
 116 GGC TAC CTG CTG CCG GTG GCC GTG GTG AGC CTG GCC TAC GGA CGC ACG 683
 117 Gly Tyr Leu Leu Pro Val Ala Val Val Ser Leu Ala Tyr Gly Arg Thr
 118 195 200 205
 120 CTA TGT TTC CTA TGG GCC GCC GTG GGT CCC GCG GGC GCG GCG GCA GCA 731
 121 Leu Cys Phe Leu Trp Ala Ala Val Gly Pro Ala Gly Ala Ala Ala Ala
 122 210 215 220
 124 GAG GCG CGC AGA CGG GCG ACC GGC CGG GCG GGA CGC GCC ATG CTG GCA 779
 125 Glu Ala Arg Arg Arg Ala Thr Gly Arg Ala Gly Arg Ala Met Leu Ala
 126 225 230 235
 128 GTG GCC GCG CTC TAC GCG CTT TGC TGG GGC CCG CAC CAC GCG CTC ATC 827

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Input Set : N:\Crf3\RULE60\10006343.raw

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129	Val	Ala	Ala	Leu	Tyr	Ala	Leu	Cys	Trp	Gly	Pro	His	His	Ala	Leu	Ile	
130	240			245				250				255					
132	CTC	TGC	TTC	TGG	TAC	GGC	CGC	TTC	GCC	TTC	AGC	CCG	GCC	ACC	TAC	GCC	875
133	Leu	Cys	Phe	Trp	Tyr	Gly	Arg	Phe	Ala	Phe	Ser	Pro	Ala	Thr	Tyr	Ala	
134				260				265				270					
136	TGT	CGC	CTG	GCC	TCG	CAC	TGC	CTC	GCC	TAC	GCC	AAC	TCC	TGC	CTT	AAC	923
137	Cys	Arg	Leu	Ala	Ser	His	Cys	Leu	Ala	Tyr	Ala	Asn	Ser	Cys	Leu	Asn	
138				275				280				285					
140	CCG	CTC	GTC	TAC	TCG	CTC	GCC	TCG	CGC	CAC	TTC	CGC	GCG	CGC	TTC	CGC	971
141	Pro	Leu	Val	Tyr	Ser	Leu	Ala	Ser	Arg	His	Phe	Arg	Ala	Arg	Phe	Arg	
142				290				295				300					
144	CGC	CTG	TGG	CCC	TGC	GGC	CGT	CGC	CGC	CAC	CGC	CAC	CAC	CGC	GCT		1019
145	Arg	Leu	Trp	Pro	Cys	Gly	Arg	Arg	Arg	His	Arg	His	His	His	Arg	Ala	
146				305				310				315					
148	CAT	CGA	GCC	CTC	CGT	CGT	GTC	CAG	CCG	GCG	TCT	TCG	GGC	CCC	GCC	GGT	1067
149	His	Arg	Ala	Leu	Arg	Arg	Val	Gln	Pro	Ala	Ser	Ser	Gly	Pro	Ala	Gly	
150	320				325				330				335				
152	TAT	CCC	GGC	GAC	GCC	AGG	CCT	CGT	GGT	TGG	AGT	ATG	GAG	CCC	AGA	GGG	1115
153	Tyr	Pro	Gly	Asp	Ala	Arg	Pro	Arg	Gly	Trp	Ser	Met	Glu	Pro	Arg	Gly	
154				340				345				350					
156	GAT	GCT	CTG	CGT	GGT	GGT	GGA	GAG	ACT	AGA	CTA	ACC	CTG	TCC	CCC	AGG	1163
157	Asp	Ala	Leu	Arg	Gly	Gly	Gly	Glu	Thr	Arg	Leu	Thr	Leu	Ser	Pro	Arg	
158				355				360				365					
160	GGA	CCT	CAA	TAACCCTGCC	CGCTTGACT	CTGACGTCTG	TCAGAATGCC										1212
161	Gly	Pro	Gln														
162		370															
164	ACCAAGGAAC	ATCTAGGGAA	CGGCAGTCTC	GCCAGGCTCC	ACCAAAAGC	AGAAGCAAAG											1272
166	TTGCAGGG																1280
169	(2)	INFORMATION	FOR	SEQ	ID	NO:	2:										
171		(i)	SEQUENCE	CHARACTERISTICS:													
172			(A)	LENGTH:	370	amino	acids										
173			(B)	TYPE:	amino	acid											
174			(D)	TOPOLOGY:	linear												
176		(ii)	MOLECULE	TYPE:	protein												
178		(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:	2:									
180	Met	Ala	Asp	Ile	Gln	Asn	Ile	Ser	Leu	Asp	Ser	Pro	Gly	Ser	Val	Gly	
181	1			5				10				15					
183	Ala	Val	Ala	Val	Pro	Val	Ile	Phe	Ala	Leu	Ile	Phe	Leu	Leu	Gly	Met	
184				20				25				30					
186	Val	Gly	Asn	Gly	Leu	Val	Leu	Ala	Val	Leu	Leu	Gln	Pro	Gly	Pro	Ser	
187				35				40				45					
189	Ala	Trp	Gln	Glu	Pro	Ser	Ser	Thr	Thr	Asp	Leu	Phe	Ile	Leu	Asn	Leu	
190				50				55				60					
192	Ala	Val	Ala	Asp	Leu	Cys	Phe	Ile	Leu	Cys	Cys	Val	Pro	Phe	Gln	Ala	
193				65				70				75				80	
195	Ala	Ile	Tyr	Thr	Leu	Asp	Ala	Trp	Leu	Phe	Gly	Ala	Phe	Val	Cys	Lys	
196				85				90				95					
198	Thr	Val	His	Leu	Leu	Ile	Tyr	Leu	Thr	Met	Tyr	Ala	Ser	Ser	Phe	Thr	
199				100				105				110					

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201 Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala Val Arg His Pro Leu
 202 115 120 125
 204 Arg Ser Arg Ala Leu Arg Thr Pro Arg Asn Ala Arg Ala Ala Val Gly
 205 130 135 140
 207 Leu Val Trp Leu Leu Ala Leu Phe Ser Ala Pro Tyr Leu Ser Tyr
 208 145 150 155 160
 210 Tyr Gly Thr Val Arg Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala Trp
 211 165 170 175
 213 Glu Asp Ala Arg Arg Ala Leu Asp Val Ala Thr Phe Ala Ala Gly
 214 180 185 190
 216 Tyr Leu Leu Pro Val Ala Val Val Ser Leu Ala Tyr Gly Arg Thr Leu
 217 195 200 205
 219 Cys Phe Leu Trp Ala Ala Val Gly Pro Ala Gly Ala Ala Ala Glu
 220 210 215 220
 222 Ala Arg Arg Arg Ala Thr Gly Arg Ala Gly Arg Ala Met Leu Ala Val
 223 225 230 235 240
 225 Ala Ala Leu Tyr Ala Leu Cys Trp Gly Pro His His Ala Leu Ile Leu
 226 245 250 255
 228 Cys Phe Trp Tyr Gly Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala Cys
 229 260 265 270
 231 Arg Leu Ala Ser His Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn Pro
 232 275 280 285
 234 Leu Val Tyr Ser Leu Ala Ser Arg His Phe Arg Ala Arg Phe Arg Arg
 235 290 295 300
 237 Leu Trp Pro Cys Gly Arg Arg Arg His Arg His His His Arg Ala His
 238 305 310 315 320
 240 Arg Ala Leu Arg Arg Val Gln Pro Ala Ser Ser Gly Pro Ala Gly Tyr
 241 325 330 335
 243 Pro Gly Asp Ala Arg Pro Arg Gly Trp Ser Met Glu Pro Arg Gly Asp
 244 340 345 350
 246 Ala Leu Arg Gly Gly Glu Thr Arg Leu Thr Leu Ser Pro Arg Gly
 247 355 360 365
 249 Pro Gln
 250 370

253 (2) INFORMATION FOR SEQ ID NO: 3:

255 (i) SEQUENCE CHARACTERISTICS:
 256 (A) LENGTH: 1417 base pairs
 257 (B) TYPE: nucleic acid
 258 (C) STRANDEDNESS: single
 259 (D) TOPOLOGY: linear

W--> 261 (ii) MOLECULE TYPE: DNA

263 (ix) FEATURE:
 264 (A) NAME/KEY: CDS
 265 (B) LOCATION: 1..1281
 268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

270 CAC TCA GCG ATG ACT TTG GCT CTG CTC TCC CCT CCT CCA TCT CCC ACG
 271 His Ser Ala Met Thr Leu Ala Leu Leu Ser Pro Pro Pro Ser Pro Thr

48

W--> 272 375 380 385
 274 AGC TTC CAG CCC AGA ACA CCT GGC CAG ACC CAG GTC GGG GGA GTT AGA

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Input Set : N:\CrF3\RULE60\10006343.raw
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275	Ser Phe Gln Pro Arg Thr Pro Gly Gln Thr Gln Val Gly Gly Val Arg				
W--> 276	390	395	400		
278	TCC CCG GGT CAA GCA ACC AGA ACT GGG GGC TCT TGC CTG AGG ATT CCA			144	
279	Ser Arg Gly Gln Ala Thr Arg Thr Gly Gly Ser Cys Leu Arg Ile Pro				
W--> 280	405	410	415		
282	GCT TCT CTT CCC AGG TGC CCG TCT GAT GGG GAG ATG GCT GAT GCC CAG			192	
283	Ala Ser Leu Pro Arg Cys Pro Ser Asp Gly Glu Met Ala Asp Ala Gln				
W--> 284	420	425	430		
286	AAC ATT TCA CTG GAC AGC CCA GGG AGT GTG GGG GCC GTG GCA GTG CCT			240	
287	Asn Ile Ser Leu Asp Ser Pro Gly Ser Val Gly Ala Val Ala Val Pro				
W--> 288	435	440	445	450	
290	GTG GTC TTT GCC CTA ATC TTC CTG CTG GGC ACA GTG GGC AAT GGG CTG			288	
291	Val Val Phe Ala Leu Ile Phe Leu Leu Gly Thr Val Gly Asn Gly Leu				
W--> 292	455	460	465		
294	GTG CTG GCA GTG CTC CTG CAG CCT GGC CCG AGT GCC TGG CAG GAG CCT			336	
295	Val Leu Ala Val Leu Leu Gln Pro Gly Pro Ser Ala Trp Gln Glu Pro				
W--> 296	470	475	480		
298	GGC AGC ACC ACG GAC CTG TTC ATC CTC AAC CTG GCG GTG GCT GAC CTC			384	
299	Gly Ser Thr Thr Asp Leu Phe Ile Leu Asn Leu Ala Val Ala Asp Leu				
W--> 300	485	490	495		
302	TGC TTC ATC CTG TGC GTG CCC TTC CAG GCC ACC ATC TAC ACG CTG			432	
303	Cys Phe Ile Leu Cys Cys Val Pro Phe Gln Ala Thr Ile Tyr Thr Leu				
W--> 304	500	505	510		
306	GAT GCC TGG CTC TTT GGG GCC CTC GTC TGC AAG GCC GTG CAC CTG CTC			480	
307	Asp Ala Trp Leu Phe Gly Ala Leu Val Cys Lys Ala Val His Leu Leu				
W--> 308	515	520	525	530	
310	ATC TAC CTC ACC ATG TAC GCC AGC AGC TTT ACG CTG GCT GCT GTC TCC			528	
311	Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe Thr Leu Ala Ala Val Ser				
W--> 312	535	540	545		
314	GTG GAC AGG TAC CTG GCC GTG CCG CAC CCG CTG CGC TCG CGC GCC CTG			576	
315	Val Asp Arg Tyr Leu Ala Val Arg His Pro Leu Arg Ser Arg Ala Leu				
W--> 316	550	555	560		
318	CGC ACG CCG CGT AAC GCC CGC GCC GCA GTG GGG CTG GTG TGG CTG CTG			624	
319	Arg Thr Pro Arg Asn Ala Arg Ala Ala Val Gly Leu Val Trp Leu Leu				
W--> 320	565	570	575		
322	GCG GCG CTC TTC TCG GCG CCC TAC CTC AGC TAC TAC GGC ACC GTG CGC			672	
323	Ala Ala Leu Phe Ser Ala Pro Tyr Leu Ser Tyr Tyr Gly Thr Val Arg				
W--> 324	580	585	590		
326	TAC GGC GCG CTG GAG CTC TGC GTG CCC GCC TGG GAG GAC GCG CGC CGC			720	
327	Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala Trp Glu Asp Ala Arg Arg				
W--> 328	595	600	605	610	
330	CGC GCC CTG GAC GTG GCC ACC TTC GCT GCC GGC TAC CTG CTG CCC GTG			768.	
331	Arg Ala Leu Asp Val Ala Thr Phe Ala Ala Gly Tyr Leu Leu Pro Val				
W--> 332	615	620	625		
334	GCT GTG GTG AGC CTG GCC TAC GGG CGC ACG CTG CGC TTC CTG TGG GCC			816	
335	Ala Val Val Ser Leu Ala Tyr Gly Arg Thr Leu Arg Phe Leu Trp Ala				
W--> 336	630	635	640		
338	GCC GTG GGT CCC GCG GGC GCG GCG GCG GAG GCG CGG CGG AGG GCG			864	
339	Ala Val Gly Pro Ala Gly Ala Ala Glu Ala Arg Arg Arg Ala				

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/006,343

DATE: 02/01/2002
TIME: 11:47:31

Input Set : N:\Crf3\RULE60\10006343.raw
Output Set: N:\CRF3\02012002\J006343.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:58 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:261 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:272 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:284 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:292 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:296 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:300 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:304 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:308 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:312 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:316 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:320 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:324 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:328 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:332 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:336 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:340 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:344 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:348 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:352 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:356 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:360 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:364 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:368 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:372 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:376 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:484 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:563 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:578 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:593 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:610 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:625 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:640 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:655 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12
L:670 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:685 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:700 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
L:715 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16
L:730 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17
L:745 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18
L:761 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19
L:776 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20
L:791 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10006343.raw
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L:809 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
L:824 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23
L:839 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:854 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:869 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:884 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:899 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:914 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:929 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:944 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:959 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:974 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33
L:989 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:1004 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35
L:1019 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36
L:1034 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37
L:1049 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=38
L:1063 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=39
L:1078 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=40
L:1093 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=41
L:1108 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=42
L:1123 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=43
L:1138 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=44
L:1153 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=45
L:1168 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=46
L:1183 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=47
L:1201 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=48
L:1216 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=49
L:1231 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=50
L:1246 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=51
L:1260 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=52